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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/842,628

DATE: 09/21/2001

TIME: 20:44:39

Input Set : A:\23032108.app

Output Set: N:\CRF3\09212001\I842628.raw

ENTERED

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3 <110> APPLICANT: ROBERTS, JOSEPH
4     MACALLISTER, THOMAS W.
5     SETHURAMAN, NATARAJAN
6     FREEMAN, ABBIE G.
8 <120> TITLE OF INVENTION: GENETICALLY ENGINEERED GLUTAMINASE AND ITS USE IN
9     ANTIVIRAL AND ANTICANCER THERAPY
11 <130> FILE REFERENCE: 023032/0108
13 <140> CURRENT APPLICATION NUMBER: 09/842,628
14 <141> CURRENT FILING DATE: 2001-04-27
16 <150> PRIOR APPLICATION NUMBER: 08/050,482
17 <151> PRIOR FILING DATE: 1995-04-25
19 <150> PRIOR APPLICATION NUMBER: PCT/US92/10421
20 <151> PRIOR FILING DATE: 1992-12-04
22 <150> PRIOR APPLICATION NUMBER: DE P 4140003.8
23 <151> PRIOR FILING DATE: 1991-12-04
25 <160> NUMBER OF SEQ ID NOS: 22
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1014
31 <212> TYPE: DNA
32 <213> ORGANISM: Pseudomonas sp.
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)..(1008)
38 <400> SEQUENCE: 1
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40 Lys Glu Val Glu Asn Gln Gln Lys Leu Ala Asn Val Val Ile Leu Ala
41   1           5           10           15
43 acc ggc ggc acc atc gcc ggc gct ggc gcc agc gcg gcc aac agc gcc   96
44 Thr Gly Gly Thr Ile Ala Gly Ala Gly Ala Ser Ala Ala Asn Ser Ala
45           20           25           30
47 acc tac cag gct gcc aag gtt ggc gtc gac aag ctg att gcc ggc gtg   144
48 Thr Tyr Gln Ala Ala Lys Val Gly Val Asp Lys Leu Ile Ala Gly Val
49           35           40           45
51 ccg gag ctg gcc gac ctg gcc aat gtg cgc ggc gag cag gtg atg cag   192
52 Pro Glu Leu Ala Asp Leu Ala Asn Val Arg Gly Glu Gln Val Met Gln
53   50           55           60
55 atc gcc tcc gaa agc atc acc aac gac gac ctg ctc aag ctg gca agc   240
56 Ile Ala Ser Glu Ser Ile Thr Asn Asp Asp Leu Leu Lys Leu Ala Ser
57  65           70           75           80
59 agc gtg gcc gag ctg gcc gac agc aat gac gtc gat ggc atc gtc atc   288
60 Ser Val Ala Glu Leu Ala Asp Ser Asn Asp Val Asp Gly Ile Val Ile
61           85           90           95
63 acc cat ggc acc gac acc ctg gaa gaa acc gcc tac ttt ttg aac ctc   336
64 Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala Tyr Phe Leu Asn Leu
65           100          105          110
67 gtg gaa aag acc gac aag ccg atc gtc gtg gtc ggt tcc atg cgc ccc   384

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68 Val Glu Lys Thr Asp Lys Pro Ile Val Val Val Gly Ser Met Arg Pro
69      115                      120                      125
71 ggc acc gcc atg tcc gcc gac ggc atg ctc aac ctg tac aac gcc gtg 432
72 Gly Thr Ala Met Ser Ala Asp Gly Met Leu Asn Leu Tyr Asn Ala Val
73      130                      135                      140
75 gcc gtg gcc agc aac aag gac tcg cgc ggc aag ggc gtg ctg gtg acc 480
76 Ala Val Ala Ser Asn Lys Asp Ser Arg Gly Lys Gly Val Leu Val Thr
77 145                      150                      155                      160
79 atg aac gac gag atc cag tcc ggg cgt gac gtg agc aag tcg atc aac 528
80 Met Asn Asp Glu Ile Gln Ser Gly Arg Asp Val Ser Lys Ser Ile Asn
81      165                      170                      175
83 atc aag acc gaa gcc ttc aag agc gcc tgg ggc ccg ctg ggc atg gtg 576
84 Ile Lys Thr Glu Ala Phe Lys Ser Ala Trp Gly Pro Leu Gly Met Val
85      180                      185                      190
87 gtg gaa ggc aag tcg tac tgg ttc cgc ctg ccg gcc aag cgc cac acg 624
88 Val Glu Gly Lys Ser Tyr Trp Phe Arg Leu Pro Ala Lys Arg His Thr
89      195                      200                      205
91 gtc aac tcc gag ttc gac atc aag cag atc agc agc ctg ccc cag gtg 672
92 Val Asn Ser Glu Phe Asp Ile Lys Gln Ile Ser Ser Leu Pro Gln Val
93      210                      215                      220
95 gac atc gcc tac agc tat ggc aac gtc acc gac acg gcc tac aag gcc 720
96 Asp Ile Ala Tyr Ser Tyr Gly Asn Val Thr Asp Thr Ala Tyr Lys Ala
97 225                      230                      235                      240
99 ctg gca cag aac ggc gcc aag gcg ctg atc cat gcc ggc acc ggc aat 768
100 Leu Ala Gln Asn Gly Ala Lys Ala Leu Ile His Ala Gly Thr Gly Asn
101      245                      250                      255
103 ggc tcg gtg tcg tcg cgg gtg gtg cca gcc ctg cag gag ctg cgc aag 816
104 Gly Ser Val Ser Ser Arg Val Val Pro Ala Leu Gln Glu Leu Arg Lys
105      260                      265                      270
107 aac ggc gtg cag atc att cgt tcg tca cgt caa cag ggc ggt ttc gtg 864
108 Asn Gly Val Gln Ile Ile Arg Ser Ser Arg Gln Gln Gly Gly Phe Val
109      275                      280                      285
111 ctg cgt aac gcc gag cag ccc gac gac aag aac gac tgg gtc gtg gcc 912
112 Leu Arg Asn Ala Glu Gln Pro Asp Asp Lys Asn Asp Trp Val Val Ala
113      290                      295                      300
115 cac gac ctg aac ccg cag aag gcc cgc atc ctg gcg atg gtg gca atg 960
116 His Asp Leu Asn Pro Gln Lys Ala Arg Ile Leu Ala Met Val Ala Met
117 305                      310                      315                      320
119 acc aag acc cag gac agc aag gag ctg cag cgc att ttc tgg gaa tac 1008
120 Thr Lys Thr Gln Asp Ser Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
121      325                      330                      335
123 tgataa 1014
126 <210> SEQ ID NO: 2
127 <211> LENGTH: 336
128 <212> TYPE: PRT
129 <213> ORGANISM: Pseudomonas sp.
131 <400> SEQUENCE: 2
132 Lys Glu Val Glu Asn Gln Gln Lys Leu Ala Asn Val Val Ile Leu Ala
133 1 5 10 15

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135 Thr Gly Gly Thr Ile Ala Gly Ala Gly Ala Ser Ala Ala Asn Ser Ala
136           20           25           30
138 Thr Tyr Gln Ala Ala Lys Val Gly Val Asp Lys Leu Ile Ala Gly Val
139           35           40           45
141 Pro Glu Leu Ala Asp Leu Ala Asn Val Arg Gly Glu Gln Val Met Gln
142           50           55           60
144 Ile Ala Ser Glu Ser Ile Thr Asn Asp Asp Leu Leu Lys Leu Ala Ser
145           65           70           75           80
147 Ser Val Ala Glu Leu Ala Asp Ser Asn Asp Val Asp Gly Ile Val Ile
148           85           90           95
150 Thr His Gly Thr Asp Thr Leu Glu Glu Thr Ala Tyr Phe Leu Asn Leu
151           100          105          110
153 Val Glu Lys Thr Asp Lys Pro Ile Val Val Val Gly Ser Met Arg Pro
154           115          120          125
156 Gly Thr Ala Met Ser Ala Asp Gly Met Leu Asn Leu Tyr Asn Ala Val
157           130          135          140
159 Ala Val Ala Ser Asn Lys Asp Ser Arg Gly Lys Gly Val Leu Val Thr
160           145          150          155          160
162 Met Asn Asp Glu Ile Gln Ser Gly Arg Asp Val Ser Lys Ser Ile Asn
163           165          170          175
165 Ile Lys Thr Glu Ala Phe Lys Ser Ala Trp Gly Pro Leu Gly Met Val
166           180          185          190
168 Val Glu Gly Lys Ser Tyr Trp Phe Arg Leu Pro Ala Lys Arg His Thr
169           195          200          205
171 Val Asn Ser Glu Phe Asp Ile Lys Gln Ile Ser Ser Leu Pro Gln Val
172           210          215          220
174 Asp Ile Ala Tyr Ser Tyr Gly Asn Val Thr Asp Thr Ala Tyr Lys Ala
175           225          230          235          240
177 Leu Ala Gln Asn Gly Ala Lys Ala Leu Ile His Ala Gly Thr Gly Asn
178           245          250          255
180 Gly Ser Val Ser Ser Arg Val Val Pro Ala Leu Gln Glu Leu Arg Lys
181           260          265          270
183 Asn Gly Val Gln Ile Ile Arg Ser Ser Arg Gln Gln Gly Gly Phe Val
184           275          280          285
186 Leu Arg Asn Ala Glu Gln Pro Asp Asp Lys Asn Asp Trp Val Val Ala
187           290          295          300
189 His Asp Leu Asn Pro Gln Lys Ala Arg Ile Leu Ala Met Val Ala Met
190           305          310          315          320
192 Thr Lys Thr Gln Asp Ser Lys Glu Leu Gln Arg Ile Phe Trp Glu Tyr
193           325          330          335
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197 <211> LENGTH: 20
198 <212> TYPE: DNA
199 <213> ORGANISM: Artificial Sequence
201 <220> FEATURE:
202 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
204 <400> SEQUENCE: 3
205 tgcagcttga gcaggtcgtc
208 <210> SEQ ID NO: 4

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Input Set : A:\23032108.app

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209 <211> LENGTH: 21
210 <212> TYPE: DNA
211 <213> ORGANISM: Artificial Sequence
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220 <210> SEQ ID NO: 5
221 <211> LENGTH: 20
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
228 <400> SEQUENCE: 5
229 cctacttttt gaacctcgtg 20
232 <210> SEQ ID NO: 6
233 <211> LENGTH: 20
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
240 <400> SEQUENCE: 6
241 caagtcgtac tggttccgcc 20
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 21
246 <212> TYPE: DNA
247 <213> ORGANISM: Artificial Sequence
249 <220> FEATURE:
250 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
252 <400> SEQUENCE: 7
253 caatcgtcct ggcgactcgt g 21
256 <210> SEQ ID NO: 8
257 <211> LENGTH: 20
258 <212> TYPE: DNA
259 <213> ORGANISM: Artificial Sequence
261 <220> FEATURE:
262 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
264 <400> SEQUENCE: 8
265 gcagatcatt cgttcgtcca 20
268 <210> SEQ ID NO: 9
269 <211> LENGTH: 20
270 <212> TYPE: DNA
271 <213> ORGANISM: Artificial Sequence
273 <220> FEATURE:
274 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
276 <400> SEQUENCE: 9
277 tgacgatgcc atcgacgtca 20
280 <210> SEQ ID NO: 10
281 <211> LENGTH: 20

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Input Set : A:\23032108.app

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282 <212> TYPE: DNA
 283 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 286 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 288 <400> SEQUENCE: 10
 289 tcacgtcacg cccggactgg 20
 292 <210> SEQ ID NO: 11
 293 <211> LENGTH: 20
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Artificial Sequence
 297 <220> FEATURE:
 298 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 300 <400> SEQUENCE: 11
 301 agctcctgca gggctggcac 20
 304 <210> SEQ ID NO: 12
 305 <211> LENGTH: 14
 306 <212> TYPE: DNA
 307 <213> ORGANISM: Artificial Sequence
 309 <220> FEATURE:
 310 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
 312 <220> FEATURE:
 313 <221> NAME/KEY: modified_base
 314 <222> LOCATION: (9)
 315 <223> OTHER INFORMATION: a, t, c, g, other or unknown
 317 <400> SEQUENCE: 12
 318 aargargtng araa 14
 321 <210> SEQ ID NO: 13
 322 <211> LENGTH: 18
 323 <212> TYPE: DNA
 324 <213> ORGANISM: Artificial Sequence
 326 <220> FEATURE:
 327 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
 329 <400> SEQUENCE: 13
 330 atggaygayg arathgar 18
 333 <210> SEQ ID NO: 14
 334 <211> LENGTH: 14
 335 <212> TYPE: DNA
 336 <213> ORGANISM: Artificial Sequence
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 339 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
 341 <400> SEQUENCE: 14
 342 athttytggg arta 14
 345 <210> SEQ ID NO: 15
 346 <211> LENGTH: 35
 347 <212> TYPE: DNA
 348 <213> ORGANISM: Artificial Sequence
 350 <220> FEATURE:
 351 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
 353 <400> SEQUENCE: 15

VERIFICATION SUMMARY

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Input Set : A:\23032108.app

Output Set: N:\CRF3\09212001\I842628.raw

L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12